

## SEQUENCE LISTING

<110> Moore, Paul A.  
 Rosen, Craig A.  
 Ruben, Steven M.

<120> Cytokine Receptor Common Gamma Chain Like

<130> PF466

<140> Unassigned  
 <141> 1999-03-05

<150> 60/086,505  
 <151> 1998-05-22

<150> 60/078,563  
 <151> 1998-03-19

<160> 30

<170> PatentIn Ver. 2.0

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ctg ctg gga ggc tgg atg gct ttg ggg caa gga gga gca gca gaa gga 99  
 Leu Leu Gly Trp Met Ala Leu Gly Gln Gly Ala Ala Glu Gly  
 15 20 25

gta cag att cag atc atc tac ttc aat tta gaa acc gtg cag gtg aca 147  
 Val Gln Ile Gln Ile Ile Tyr Phe Asn Leu Glu Thr Val Gln Val Thr  
 30 35 40 45

tgg aat gcc agc aaa tac tcc agg acc aac ctg act ttc cac tac aga 195  
 Trp Asn Ala Ser Lys Tyr Ser Arg Thr Asn Leu Thr Phe His Tyr Arg  
 50 55 60

ttc aac ggt gat gag gcc tat gac cag tgc acc aac tac ctt ctc cag 243  
 Phe Asn Gly Asp Glu Ala Tyr Asp Gln Cys Thr Asn Tyr Leu Leu Gln  
 65 70 75

gaa ggt cac act tcg ggg tgc ctc cta gac gca gag cag cga gac gac 291  
 Glu Gly His Thr Ser Gly Cys Leu Leu Asp Ala Glu Gln Arg Asp Asp  
 80 85 90

att ctc tat ttc tcc atc agg aat ggg acg cac ccc gtt ttc acc gca 339  
 Ile Leu Tyr Phe Ser Ile Arg Asn Gly Thr His Pro Val Phe Thr Ala  
 95 100 105

agt cgc tgg atg gtt tat tac ctg aaa ccc agt tcc ccg aag cac gtg 387  
 Ser Arg Trp Met Val Tyr Tyr Leu Lys Pro Ser Ser Pro Lys His Val  
 110 115 120 125

aga ttt tgc tgg cat cag gat gca gtg acg gtg acg tgt tct gac ctg 435  
 Arg Phe Ser Trp His Gln Asp Ala Val Thr Val Thr Cys Ser Asp Leu  
 130 135 140

tcc tac ggg gat ctc ctc tat gag gtt cag tac cgg agc ccc ttc gac 483  
 Ser Tyr Gly Asp Leu Leu Tyr Glu Val Gln Tyr Arg Ser Pro Phe Asp  
 145 150 155

acc gag tgg cag tcc aaa cag gaa aat acc tgc aac gtc acc ata gaa 531  
 Thr Glu Trp Gln Ser Lys Gln Glu Asn Thr Cys Asn Val Thr Ile Glu  
 160 165 170

ggc ttg gat gcc gag aag tgt tac tct ttc tgg gtc agg gtg aag gct 579  
 Gly Leu Asp Ala Glu Lys Cys Tyr Ser Phe Trp Val Arg Val Lys Ala  
 175 180 185

atg gag gat gta tat ggg cca gac aca tac cca agc gac tgg tca gag 627  
 Met Glu Asp Val Tyr Gly Pro Asp Thr Tyr Pro Ser Asp Trp Ser Glu  
 190 195 200 205

gtg aca tgc tgg cag aga ggc gag att cgg gat gcc tgt gca gag aca 675  
 Val Thr Cys Trp Gln Arg Gly Glu Ile Arg Asp Ala Cys Ala Glu Thr  
 210 215 220

cca acg cct ccc aaa cca aag ctg tcc aaa ttt att tta att tcc agc 723  
 Pro Thr Pro Pro Lys Pro Lys Leu Ser Lys Phe Ile Leu Ile Ser Ser  
 225 230 235

ctg gcc atc ctt ctg atg gtg tct ctc ctc ctt ctg tct tta tgg aaa 771  
 Leu Ala Ile Leu Leu Met Val Ser Leu Leu Leu Ser Leu Trp Lys  
 240 245 250

tta tgg aga gtg aag aag ttt ctc att ccc agc gtg cca gac ccg aaa 819  
 Leu Trp Arg Val Lys Lys Phe Leu Ile Pro Ser Val Pro Asp Pro Lys  
 255 260 265

tcc atc ttc ccc ggg ctc ttt gag ata cac caa ggg aac ttc cag gag 867  
 Ser Ile Phe Pro Gly Leu Phe Glu Ile His Gln Gly Asn Phe Gln Glu  
 270 275 280 285

tgg atc aca gac acc cag aac gtg gcc cac ctc cac aag atg gca ggt 915  
 Trp Ile Thr Asp Thr Gln Asn Val Ala His Leu His Lys Met Ala Gly  
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gca gag caa gaa agt ggc ccc gag gag ccc ctg gta gtc cag ttg gcc 963  
 Ala Glu Gln Glu Ser Gly Pro Glu Glu Pro Leu Val Val Gln Leu Ala  
 305 310 315

aag act gaa gcc gag tct ccc agg atg ctg gac cca cag acc gag gag 1011  
 Lys Thr Glu Ala Glu Ser Pro Arg Met Leu Asp Pro Gln Thr Glu Glu  
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aaa gag gcc tct ggg gga tcc ctc cag ctt ccc cac cag ccc ctc caa 1059  
 Lys Glu Ala Ser Gly Gly Ser Leu Gln Leu Pro His Gln Pro Leu Gln  
 335 340 345

ggc ggt gat gtg gtc aca atc ggg ggc ttc acc ttt gtg atg aat gac 1107  
 Gly Gly Asp Val Val Thr Ile Gly Gly Phe Thr Phe Val Met Asn Asp  
 350 355 360 365

cgc tcc tac gtg gcg ttg tgatggacac accactgtca aagtcaacgt 1155  
 Arg Ser Tyr Val Ala Leu  
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caggatccac gttgacattt aaagacagag gggactgtcc cggggactcc acaccaccat 1215  
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 Gln Ile Ile Tyr Phe Asn Leu Glu Thr Val Gln Val Thr Trp Asn Ala  
 35 40 45  
 Ser Lys Tyr Ser Arg Thr Asn Leu Thr Phe His Tyr Arg Phe Asn Gly  
 50 55 60  
 Asp Glu Ala Tyr Asp Gln Cys Thr Asn Tyr Leu Leu Gln Glu Gly His  
 65 70 75 80  
 Thr Ser Gly Cys Leu Leu Asp Ala Glu Gln Arg Asp Asp Ile Leu Tyr  
 85 90 95  
 Phe Ser Ile Arg Asn Gly Thr His Pro Val Phe Thr Ala Ser Arg Trp  
 100 105 110  
 Met Val Tyr Tyr Leu Lys Pro Ser Ser Pro Lys His Val Arg Phe Ser  
 115 120 125  
 Trp His Gln Asp Ala Val Thr Val Thr Cys Ser Asp Leu Ser Tyr Gly  
 130 135 140  
 Asp Leu Leu Tyr Glu Val Gln Tyr Arg Ser Pro Phe Asp Thr Glu Trp  
 145 150 155 160

Gln Ser Lys Gln Glu Asn Thr Cys Asn Val Thr Ile Glu Gly Leu Asp  
 165 170 175  
 Ala Glu Lys Cys Tyr Ser Phe Trp Val Arg Val Lys Ala Met Glu Asp  
 180 185 190  
 Val Tyr Gly Pro Asp Thr Tyr Pro Ser Asp Trp Ser Glu Val Thr Cys  
 195 200 205  
 Trp Gln Arg Gly Glu Ile Arg Asp Ala Cys Ala Glu Thr Pro Thr Pro  
 210 215 220  
 Pro Lys Pro Lys Leu Ser Lys Phe Ile Leu Ile Ser Ser Leu Ala Ile  
 225 230 235 240  
 Leu Leu Met Val Ser Leu Leu Leu Leu Ser Leu Trp Lys Leu Trp Arg  
 245 250 255  
 Val Lys Lys Phe Leu Ile Pro Ser Val Pro Asp Pro Lys Ser Ile Phe  
 260 265 270  
 Pro Gly Leu Phe Glu Ile His Gln Gly Asn Phe Gln Glu Trp Ile Thr  
 275 280 285  
 Asp Thr Gln Asn Val Ala His Leu His Lys Met Ala Gly Ala Glu Gln  
 290 295 300  
 Glu Ser Gly Pro Glu Glu Pro Leu Val Val Gln Leu Ala Lys Thr Glu  
 305 310 315 320  
 Ala Glu Ser Pro Arg Met Leu Asp Pro Gln Thr Glu Glu Lys Glu Ala  
 325 330 335  
 Ser Gly Gly Ser Leu Gln Leu Pro His Gln Pro Leu Gln Gly Gly Asp  
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 355 360 365  
 Val Ala Leu  
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 20 25 30  
 Thr Ser Thr Pro Ala Gly Thr Leu Asp Val Ser Thr Leu Pro Leu Pro  
 35 40 45  
 Lys Val Gln Cys Phe Val Phe Asn Val Glu Tyr Met Asn Cys Thr Trp  
 50 55 60

Asn Ser Ser Ser Glu Pro Gln Pro Asn Asn Leu Thr Leu His Tyr Gly  
 65 70 75 80  
 Tyr Arg Asn Phe Asn Gly Asp Asp Lys Leu Gln Glu Cys Gly His Tyr  
 85 90 95  
 Leu Phe Ser Glu Gly Ile Thr Ser Gly Cys Trp Phe Gly Lys Lys Glu  
 100 105 110  
 Ile Arg Leu Tyr Glu Thr Phe Val Val Gln Leu Gln Asp Pro Arg Glu  
 115 120 125  
 His Arg Lys Gln Pro Lys Gln Met Leu Lys Leu Gln Asp Leu Val Ile  
 130 135 140  
 Pro Trp Ala Pro Glu Asn Leu Thr Leu Arg Asn Leu Ser Glu Phe Gln  
 145 150 155 160  
 Leu Glu Leu Ser Trp Ser Asn Arg Tyr Leu Asp His Cys Leu Glu His  
 165 170 175  
 Leu Val Gln Tyr Arg Ser Asp Arg Asp Arg Ser Trp Thr Glu Gln Ser  
 180 185 190  
 Val Asp His Arg His Ser Phe Ser Leu Pro Ser Val Asp Ala Gln Lys  
 195 200 205  
 Leu Tyr Thr Phe Arg Val Arg Ser Arg Tyr Asn Pro Leu Cys Gly Ser  
 210 215 220  
 Ala Gln His Trp Ser Asp Trp Ser Tyr Pro Ile His Trp Gly Ser Asn  
 225 230 235 240  
 Thr Ser Lys Glu Asn Ile Glu Asn Pro Glu Asn Pro Ser Leu Phe Ala  
 245 250 255  
 Leu Glu Ala Val Leu Ile Pro Leu Gly Ser Met Gly Leu Ile Val Ser  
 260 265 270  
 Leu Ile Cys Val Tyr Cys Trp Leu Glu Arg Thr Met Pro Arg Ile Pro  
 275 280 285  
 Thr Leu Lys Asn Leu Glu Asp Leu Val Thr Glu Tyr Gln Gly Asn Phe  
 290 295 300  
 Ser Ala Trp Ser Gly Val Ser Lys Gly Leu Ala Glu Ser Leu Gln Pro  
 305 310 315 320  
 Asp Tyr Ser Glu Arg Leu Cys His Val Ser Glu Ile Pro Pro Lys Gly  
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 tctcccgagc tcttgaggtc acatgcgtgg tggtagacgt aagccacgaa gaccctgagg 180  
 tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg 240  
 aggagcagta caacagcacg tacctgtgtg tcagcgtcct caccgtcctg caccaggact 300  
 ggctgaatgg caaggagtac aagtgaagg tctccaacaa agccctccca acccccatcg 360  
 agaaaacat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420  
 catcccgga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc aaaggcttct 480  
 atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac aactacaaga 540  
 ccacgcctcc cgtgctggac tccgacggct ccttcttct ctacagcaag ctcaccgtgg 600  
 acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggctctgc 660  
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 gactctagag gat 733

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 <222> (3)  
 <223> Xaa equals any amino acid

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 Trp Ser Xaa Trp Ser  
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 <213> Homo sapiens

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 cccgaaatat ctgccatctc aattag 86

<210> 7  
 <211> 27

<212> DNA  
 <213> Homo sapiens

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27

<210> 8  
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 <212> DNA  
 <213> Homo sapiens

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 gccctaact ccgcccagtt ccgcccattc tccgcccatt ggctgactaa ttttttttat 180  
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 ttttggaggc ctaggctttt gcaaaaagct t

271

<210> 9  
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<400> 9  
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32

<210> 10  
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 <212> DNA  
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<400> 10  
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31

<210> 11  
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 <212> DNA  
 <213> Homo sapiens

<400> 11  
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12

<210> 12  
 <211> 73  
 <212> DNA  
 <213> Homo sapiens

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 ccatctcaat tag

73

<210> 13  
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 <213> Homo sapiens

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 cagttccgcc cattctccgc cccatggctg actaattttt tttatttatg cagaggccga 180  
 ggccgcctcg gcctctgagc tattccagaa gtagtgagga ggcttttttg gaggcctagg 240  
 cttttgcaaa aagctt 256

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<210> 15  
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 <212> DNA  
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<400> 15  
 ggtaaagat ctcaacgcca cgtaggagcg gtc 33

<210> 16  
 <211> 38  
 <212> DNA  
 <213> Homo sapiens

<400> 16  
 ccggttagat ctgccatcat ggctttgggg caaggagg 38

<210> 17  
 <211> 36  
 <212> DNA  
 <213> Homo sapiens

<400> 17  
 ccggtttcta gatcacaagg ccacgtagga gcggtc 36

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 <212> PRT  
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 <222> (1)  
 <223> Xaa equals Ser, Thr, Gly or Leu

<220>  
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 <222> (2)  
 <223> Xaa equals any amino acid

<220>  
 <221> SITE  
 <222> (4)  
 <223> Xaa equals Ser or Gly

<220>  
 <221> SITE  
 <222> (5)  
 <223> Xaa equals any amino acid

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 Xaa Xaa Trp Xaa Xaa Trp Ser  
 1 5

<210> 19  
 <211> 7  
 <212> PRT  
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<220>  
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 <223> Xaa equals any amino acid

<220>  
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 Thr Xaa Pro Ser Xaa Trp Ser  
 1 5

<210> 20  
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 <213> Homo sapiens

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 <222> (3)  
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 <222> (4)  
 <223> Xaa equals Val or Ile

<220>  
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 <222> (6)  
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 1 5

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 Asn Ala Ser Lys Tyr Ser Arg Thr Asn Leu Thr Phe His Tyr Arg Phe  
 20 25 30  
 Asn Gly Asp Glu Ala Tyr Asp Gln Cys Thr Asn Tyr Leu Leu Gln Glu  
 35 40 45

Gly His Thr Ser Gly Cys  
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<210> 23  
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 <212> PRT  
 <213> Homo sapiens

<400> 23  
 Arg Arg His Ser Leu Phe Leu His Gln Glu Trp Asp Ala Pro Arg Phe  
 1 5 10 15

His Arg Lys Ser Leu Asp Gly Leu Leu Pro Glu Thr Gln Phe  
 20 25 30

<210> 24  
 <211> 81  
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 <213> Homo sapiens

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             20                    25                    30  
 Glu Lys Cys Tyr Ser Phe Trp Val Arg Val Lys Ala Met Glu Asp Val  
             35                    40                    45  
 Tyr Gly Pro Asp Thr Tyr Pro Ser Asp Trp Ser Glu Val Thr Cys Trp  
             50                    55                    60  
 Gln Arg Gly Glu Ile Arg Asp Ala Cys Ala Glu Thr Pro Thr Pro Pro  
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Lys

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             20                    25                    30  
 Pro Thr Pro Pro Lys Pro Lys Leu Ser Lys Phe Ile Leu Ile Ser Ser  
             35                    40                    45  
 Leu Ala Ile Leu Leu Met Val Ser Leu Leu Leu Leu Ser Leu Trp Lys  
     50                    55                    60

Leu Trp Arg Xaa Lys Lys Phe Leu Xaa Pro Ser Val Pro Asp Pro Lys  
65 70 75 80

Ser Ile Phe Pro Gly Leu Phe Xaa Ile His Gln Gly Asn Phe Gln Glu  
85 90 95

Trp Ile Thr Asp Thr Gln Asn Val Ala His Leu His Lys Met Ala Gly  
100 105 110

Ala Glu Gln Glu Ser Gly Pro Glu Glu Pro Leu Val Val Gln Leu Ala  
115 120 125

Lys Thr Glu Ala Glu Ser Pro Arg Met Leu Asp Pro Gln Thr Glu Glu  
130 135 140

Lys Glu Ala Ser Gly Gly Ser Leu Gln Leu Pro His Gln Pro Leu Gln  
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Gly Gly Asp Val Val Thr Ile Gly Gly Phe Thr Phe Val Met Asn Asp  
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Arg Ser Tyr Val Ala  
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<212> DNA

<213> Homo sapiens

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<221> misc\_feature

<222> (416)

<223> y equals c or t

<220>

<221> misc\_feature

<222> (784)

<223> m equals a or c

<220>

<221> misc\_feature

<222> (785)

<223> y equals c or t

<400> 26

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agaaaccgtg caggtgacat ggaatgccag caaatactcc aggaccaacc tgactttcca 180

ctacagattc aacggtgatg aggcctatga ccagtgcacc aactaccttc tccaggaagg 240

tcacacttcg gggtgcctcc tagacgcasa gcagcgagac gacattctct atttctccat 300

caggaatggg acgcaccccg ttttcaccgc aagtcgctgg atggtttatt acctgaaacc 360  
 cagttccccc aagcacgtga gatttcgtgg catcaggaaw gacggtgacg tgttcycgac 420  
 ctgtcctacg gggatctcct ctatgagggt cagtaccgga gcccttcga caccgagtgg 480  
 cagtccaaac aggaaaatac ctgcaacgtc accatagaag gcttggatgc cgagaagtgt 540  
 tactctttct gggtcagggt gaaggctatg gaggatgtat atgggccaga cacataccca 600  
 agcgactggt cagaggtgac atgctggcag agaggcgaga ttcgggatgc ctgtgcagag 660  
 acaccaacgc ctcccaaacc aaagctgtcc aaatttattt taatttcag cctggccatc 720  
 cttctgatgg tgtctctcct cttctgtct ttatggaaat tatggagart gaagaagttt 780  
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 gggaacttcc aggagtggat cacagacacc cagaacgtgg ccacactcca caagatggca 900  
 ggtgcagagc aagaaagtgg ccccgaggag cccctggtag tccagttggc caagactgaa 960  
 gccgagtctc ccaggatgct ggaccacag accgaggaga aagaggcctc tgggggatcc 1020  
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 aggttgatg gcagatggga gccaatgct ccaggagatt tactccaggt tccttttcgt 1380  
 gctgaacgtt gtcacataaa cccaaggca gcacgtcaa aatgctgtaa aaccatcttc 1440  
 ccactctgtg agtccccagt tccgtccatg taccattccc atagcattgg attctcggag 1500  
 gattttttgt ctgttttgag actccaaacc acctctacc ctacaaaaa aaaaaaaaaa 1560  
 aactcga 1567

<210> 27  
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<220>  
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<400> 27

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Gly Trp Met Ala Leu Gly Gln Gly Gly Ala Ala Glu Gly Val Gln Ile  
 20 25 30

Gln Ile Ile Tyr Phe Asn Leu Glu Thr Val Gln Val Thr Trp Asn Ala  
 35 40 45

Ser Lys Tyr Ser Arg Thr Asn Leu Thr Phe His Tyr Arg Phe Asn Gly  
 50 55 60

Asp Glu Ala Tyr Asp Gln Cys Thr Asn Tyr Leu Leu Gln Glu Gly His  
 65 70 75 80

Thr Ser Gly Cys Leu Leu Asp Ala Xaa Gln Arg Asp Asp Ile Leu Tyr  
 85 90 95

Phe Ser Ile Arg Asn Gly Thr His Pro Val Phe Thr Ala Ser Arg Trp  
 100 105 110

Met Val Tyr Tyr Leu Lys Pro Ser Ser Pro Lys His Val Arg Phe Arg  
 115 120 125

Gly Ile Arg Xaa Asp Gly Asp Val Phe Xaa Thr Cys Pro Thr Gly Ile  
 130 135 140

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 145 150 155 160

Pro Asn Arg Lys Ile Pro Ala Thr Ser Pro  
 165 170

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 <212> DNA  
 <213> Homo sapiens

<400> 28  
 ccggttagat ctgccatcat ggggcggctg gttctg

36

<210> 29  
 <211> 31  
 <212> DNA  
 <213> Homo sapiens

<400> 29  
 ggccggtcta gatttggaca gctttggttt g

31

<210> 30

<211> 4  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SITE  
<222> (2)  
<223> Xaa equals any amino acid

<400> 30  
Trp Xaa Trp Ser  
1

Trp Xaa Trp Ser  
1